# IN THE UNITED STATES RECEIVING OFFICE (RO/US)

## BOX PCT

FACSIMILE OF PAPER COPIES TO: 305-7937

HAND CARRY TO: Special Programs Examiner Tsang Crystal Mall 1, 7th Floor Patent & Trademark Office 1911 South Clark Place Arlington, VA 22202

In re International Patent Application of

DUKE UNIVERSITY ET AL

Agent's File Ref: 1579-379

International Application No: PCT/US99/17678

International Filing Date: 05 August 1999

For: URATE OXIDASE

15 February 2000

United States Receiving Office Honorable Commissioner of Patents and Trademarks Washington, D.C. 20231

# Response to Telephonic Request

Dear Sirs,

Responsive to Examiner Tsang's telephonic request of February 15, 2000, made to the undersigned, attached is a further paper and computer readable copy of the Sequence Listing filed November 19, 1999, along with a copy of the Applicants' Response of November 19, 1999 and date stamped post card Receipt from the submission of November 19, 1999.

In accordance with 37 CFR 1.821-1.825, I hereby state that the content of the paper and computer-readable copies of the sequence listing submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are the same. I hereby state that the submission, filed in accordance with 37 CFR 1.821(g), does not introduce new matter.

The Examiner is requested to contact the undersigned if anything further is required. A Search of all of the claims is requested.

Respectfully submitted,

NIXON & VANDERHYE P.C.

B. J. Sadoff

ney No 3666

8th Floor 1100 North Glebe Road Arlington, Virginia 22201-4714

#### SEQUENCE LISTING

<110> HERSHFIELD, MICHAEL S. KELLY, SUSAN J.										
<120> URATE OXIDASE										
<130> 1579~379										
<140> PCT/US99/17678 < 141> 1999-08-05										
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<170> PatentIn Ver. 2.0										
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cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa 144 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln 35 40 45										
ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat 192 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp 50 55 60										
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ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag 288 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu 85 90 95										
cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg 336 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val 100 105 110										
gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc 384 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val 115 120 125										
cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa 432 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 130 135 140										
cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta 480										

Gln 145	Ile	Arg	Asn	Gly	Pro 150	Pro	Val	Ile	His	Ser 155	Gly	Ile	Lys	Asp	Leu 160		•	
	gtc Val															528		
_	ttc Phe					_		_	_		-		-			576		
	tac Tyr	_			_			_		_	_		_			624		
_	acc Thr 210		-		_		_			_	_			_		672		
	tat Tyr	-									_	-				720		
_	atc Ile	_				_	-	-	-				_	_	_	768		
-	atc Ile	_	_						ttc			_	_			816		
_	ggt Gly	-			_	_	_	_	_	_			-			864		
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tga																915		
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Val	Arg	Thr	Gly 20	Tyr	Gly	Lys	Asp	Met 25	Ile	Lys	Val	Leu	His 30	Ile	Gln			
Arg	Asp	Gly 35	Lys	Tyr	His	Ser	Ile 40	Lys	Glu	Val	Ala	Thr 45	Ser	Val	Gln			
Leu	Thr 50	Leu	Ser	Ser	Lys	Lys 55	Asp	Tyr	Leu	His	Gly 60	Asp	Asn	Ser	Asp			
Val 65	Ile	Pro	Thr	Asp	Thr 70	Ile	Lys	Asn	Thr	Val 75	Asn	Val	Leu	Ala	Lys 80			
Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Thr	Phe	Ala	Val	Thr	Ile	Cys	Glu			

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85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val 105 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 135 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu 200 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met 250 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys 260 265 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu <210> 3 <211> 915 <212> DNA <213> Artificial Sequence <220> <221> CDS <222> (1)..(915) <223> Description of Artificial Sequence:pks chimera <400> 3 atg gct cat tac cgt aat gac tac aaa aag aat gat gag gta gag ttt Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe 10 gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln 25 cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln

40

ctg Leu	act Thr 50	ttg Leu	agc Ser	tcc Ser	aaa Lys	aaa Lys 55	gat Asp	tac Tyr	ctg Leu	cat His	gga Gly 60	gac Asp	aat Asn	tca Ser	gat Asp	192
gtc Val 65	atc Ile	cct Pro	aca Thr	gac Asp	acc Thr 70	atc Ile	aag Lys	aac Asn	aca Thr	gtt Val 75	aat Asn	gtc Val	ctg Leu	gcg Ala	aag Lys 80	240
ttc Phe	aaa Lys	ggc Gly	atc Ile	aaa Lys 85	agc Ser	ata Ile	gaa Glu	act Thr	ttt Phe 90	gct Ala	gtg Val	act Thr	atc Ile	tgt Cys 95	gag Glu	288
cat His	ttc Phe	ctt Leu	tct Ser 100	tcc Ser	ttc Phe	aag Lys	cat His	gtc Val 105	atc Ile	aga Arg	gct Ala	caa Gln	gtc Val 110	tat Tyr	gtg Val	336
gaa Glu	gaa Glu	gtt Val 115	cct Pro	tgg Trp	aag Lys	cgt Arg	ttt Phe 120	gaa Glu	aag Lys	aat Asn	gga Gly	gtt Val 125	aag Lys	cat His	gtc Val	384
cat His	gca Ala 130	ttt Phe	att Ile	tat Tyr	act Thr	cct Pro 135	act Thr	gga Gly	acg Thr	cac His	ttc Phe 140	tgt Cys	gag Glu	gtt Val	gaa Glu	432
cag Gln 145	ata Ile	agg Arg	aat Asn	gga Gly	cct Pro 150	cca Pro	gtc Val	att Ile	cat His	tct Ser 155	gga Gly	atc Ile	aaa Lys	gac Asp	cta Leu 160	480
aaa Lys	gtc Val	ttg Leu	aaa Lys	aca Thr 165	acc Thr	cag Gln	tct Ser	ggc Gly	ttt Phe 170	gaa Glu	gga Gly	ttc Phe	atc Ile	aag Lys 175	gac Asp	528
cag Gln	ttc Phe	acc Thr	acc Thr 180	ctc Leu	cct Pro	gag Glu	gtg Val	aag Lys 185	gac Asp	cgg Arg	tgc Cys	ttt Phe	gcc Ala 190	acc Thr	caa Gln	576
gtg Val	tac Tyr	tgc Cys 195	aaa Lys	tgg Trp	cgc Arg	tac Tyr	cac His 200	cag Gln	ggc	aga Arg	gat Asp	gtg Val 205	gac Asp	ttt Phe	gag Glu	624
gcc Ala	acc Thr 210	tgg Trp	gac Asp	act Thr	gtt Val	agg Arg 215	agc Ser	att Ile	gtc Val	ctg Leu	cag Gln 220	aaa Lys	ttt Phe	gct Ala	Gly	672
ccc Pro 225	tat Tyr	gac Asp	aaa Lys	ggc Gly	gag Glu 230	tac Tyr	tcg Ser	ccc Pro	tct Ser	gtc Val 235	cag Gln	aag Lys	aca Thr	ctc Leu	tat Tyr 240	720
gac Asp	atc Ile	cag Gln	gtg Val	ctc Leu 245	acc Thr	ctg Leu	ggc Gly	cag Gln	gtt Val 250	cct Pro	gag Glu	ata Ile	gaa Glu	gat Asp 255	atg Met	768
gaa Glu	atc Ile	agc Ser	ctg Leu 260	cca Pro	aat Asn	att Ile	cac His	tac Tyr 265	tta Leu	aac Asn	ata Ile	gac Asp	atg Met 270	tcc Ser	aaa Lys	816
atg Met	gga Gly	ctg Leu 275	atc Ile	aac Asn	aag Lys	gaa Glu	gag Glu 280	gtc Val	ttg Leu	cta Leu	cct Pro	tta Leu 285	gac Asp	aat Asn	cca Pro	864
tat Tyr	gga Gly 290	aaa Lys	att Ile	act Thr	ggt Gly	aca Thr 295	gtc Val	aag Lys	agg Arg	aag Lys	ttg Leu 300	Ser	tca Ser	aga Arg	ctg Leu	912
tga										•						915

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<211> 304

<212> PRT

<213> Artificial Sequence

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Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
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Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp 50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu 85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val 100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val 115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly 210 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr 225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met 245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu 290 295 300 <210> 5 <211> 304 <212> PRT <213> Artificial Sequence <223> Description of Artificial Sequence:baboon D3H Met Ala His Tyr His Asn Asn Tyr Lys Lys Asn Asp Glu Leu Glu Phe Val Arg Thr Gly Tyr Gly Lys Asp Met Val Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val 105 Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 135 Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 170 165 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly 215 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met 250 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys 265 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Pro Leu Asp Asn Pro

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu

<210> 6 <211> 304 <212> PRT <213> baboon <400> 6 Met Ala Asp Tyr His Asn Asn Tyr Lys Lys Asn Asp Glu Leu Glu Phe Val Arg Thr Gly Tyr Gly Lys Asp Met Val Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val 105 100 Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 135 Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu 150 155 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 170 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu 200 Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys 260 265 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Pro Leu Asp Asn Pro

280

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu 290 295 300

<210> 7 <211> 304 <212> PRT <213> pig <400> 7 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val 105 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val 120 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 135 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln 185 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu 200 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly 215 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gin Lys Thr Leu Tyr 230 Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro 275 280 285

Tyr Gly Arg Ile Thr Gly Thr Val Lys Arg Lys Leu Thr Ser Arg Leu 290 295 300

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Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly 275 280 285

Thr Val Lys Arg Lys Leu Ser Ser Arg Leu 290 295

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<220>

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Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp 50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu 85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val 100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val 115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln 180 185

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu 195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly 210 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr 225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met

Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Pro Leu Asp Asn Pro 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser 290 295 300

<210> 10

<211> 298

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PKS carboxy truncated

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Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe Val Arg Thr Gly Tyr Gly 1 5 10 15

Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His 20 25 30

Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys 35 40 45

Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr 50 55 60

Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser 65 70 75 80

Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe 85 90 95

Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys
100 105 110

Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr 115 120 125

Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro

Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr 145 150 155 160

Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro 165 170 175

Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg 180 185 190

Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val 195 200 205

Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu 210 215 220

Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Thr

225	230	235	240
225	430	433	240

Leu Gly Gln Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn 245 250 255

Ile His Tyr Leu Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys 260 265 270

Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly 275 280 285

Thr Val Lys Arg Lys Leu Ser Ser Arg Leu 290 295

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<223> Description of Artificial Sequence: PKS carboxy truncated

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Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe 1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Glu 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp 50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu 85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val 115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly 215

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met 270

Met Gly Leu Ile Asn Lys Glu Glu Glu Val Leu Leu Pro Leu Asp Asp Pro 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser 300



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-	PCTT US 99117678  Dake Univertify  PCT 10399117678  Amendment  Amendment  Pages Specification  Claims Sheets Drawings: Formal  Claims Sheets Drawings: Formal  Assignment  Assignment  Priority Document  Priority Document  Priority Document  Assignment  Fee (Check)  Fee (Check)  Fee (Check)  Fee (Check)	
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	Serial No.: PCTT US99117678  Applicant: Cake University  Amendment Pages Specification Pages Specification Sheets Drawings: S	

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# IN THE UNITED STATES RECEIVING OFFICE (RO/US)

### **BOX PCT**



In re International Patent Application of

DUKE UNIVERSITY ET AL

Agent's File Ref: 1579-379

International Application No: PCT/US99/17678

International Filing Date: 05 August 1999

For: URATE OXIDASE

19 November 1999

United States Receiving Office Honorable Commissioner of Patents and Trademarks Washington, D.C. 20231

## Response to Correct Defects in International Application

Dear Sirs.

Attached is a printed sequence listing for this application and a copy of the computer readable form on a 3.5" disk in the attached envelope.

In accordance with 37 CFR 1.821-1.825, I hereby state that the content of the paper and computer-readable copies of the sequence listing submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are the same. I hereby state that the submission, filed in accordance with 37 CFR 1.821(g), does not introduce new matter.

Respectfully submitted,

NIXON & VANDERHYE P.C.

8th Floor 1100 North Glebe Road Arlington, Virginia 22201-4714